

AMENDMENTS TO THE CLAIMS:

Claims 3-5, 7-9, 11-13, 15-17 and 27-28 are canceled without prejudice or disclaimer. The following is the status of the claims of the above-captioned application, as amended.

Claim 1 (Original). A variant of a parent Glycoside Hydrolase Family 53 galactanase, comprising an alteration in at least one of the following positions: -6, -4, -2, 1, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 20, 22, 24, 25, 26, 29, 30, 31, 32, 36, 39, 40, 41, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 54a, 54e, 54f, 54g, 54h, 55, 56, 57, 58, 61, 62, 65, 69, 77, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 101, 106, 107, 110, 113, 114, 126, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 144, 145, 146, 147, 150, 153, 157, 159, 163, 169, 171, 172, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 191, 192, 194, 198, 200, 203, 204, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 252, 252d, 252e, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 273, 274, 276, 277, 280, 283, 284, 286, 288, 288a, 289, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 302a, 302d, 302j, 302k, 302m, 302n, 302o, 302q, 302r, 302s, 302t, 302u, 302v, 302x, 302y, 302z, 302aa, 302bb, 302cc, 302dd, 302ee, 302ff, 302gg, 302hh, 302ii, 302jj, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, and 330; wherein

- (a) the alteration(s) are independently
 - (i) an insertion of an amino acid immediately downstream of the position,
 - (ii) a deletion of the amino acid which occupies the position, and/or
 - (iii) a substitution of the amino acid which occupies the position; and
- (b) the variant has galactanase activity.

Claim 2 (Original). The variant of claim 1, wherein the variant comprises at least one of the following substitutions: -6P; -4P; -2P; 1P; 3P; 5A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
6A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 7A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
8A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 9A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
10A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 11A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
12A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 13A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
14A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 15A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
16A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 18A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
20A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 22A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

24C,P; 25P; 26P; 29P; 30C; 31P; 32A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 36A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 39C; 40C; 41P;
 43A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 44A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 45A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 46A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 47A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 48A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 49A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 50A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 51A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 52A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 53A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 54A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 54aP; 54eA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 54fA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 54gA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 54hA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 55A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 56A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 57A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 58A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 61A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 62C;
 65C; 69C; 77A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 79A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 80A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 81A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 82A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 83A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 84A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 85A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 86A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 87A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 88A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 89A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 91A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 92A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 93A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 94A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 95A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 96A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 97P;
 101P; 106C; 107H,S; 110C; 113C; 114C; 126E; 131A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 133A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 134A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 135A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 136A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 137A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 139A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 140A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 141A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 142A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 144P;
 146A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 147P; 150C; 159C; 163C; 169P; 171P; 172P;
 178A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 179A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 180A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 181A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 182A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 183A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 184A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 185A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

186A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 188A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 191A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 210A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 212A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 214A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 216A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 217A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 219A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 221A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 223A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 225A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 227A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 229A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 231A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 233A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 241A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 243A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
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 247A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 249A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 252A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 252eA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 254A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 256A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 258A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 260A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 262A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 264A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 266P;
 276A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 280A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 286P;
 288P;
 288aP;
 289P;
 294A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 187A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 189A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 194C;
 198P;
 200P;
 203P;
 204P;
 211A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 213A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 215A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 216FVASTG;
 218A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 220A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 222A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 224A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 226A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 228A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 230A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 232A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 234C;
 242A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 244A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 246A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 248A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 250A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 252dA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 253A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 255A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 257A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 259A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 261A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 263A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 265A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 274C;
 277A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 283A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 293A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 295A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

296A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 297A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 298A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 299A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 300A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 301A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302aA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302dP; 302jA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302kA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302mA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302nA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302oA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302qA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302rA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302sA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302tA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302uA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302vA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302xA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302yA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302zA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302aaA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302bbA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302ccP;
 302ddA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302eeA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302ffA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302ggA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302hhA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 302iiA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 302jjA,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 303A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 304A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 305A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 306A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 307A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 308A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 309A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 310A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 311A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 312A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 313A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 314A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 315A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 316A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 317A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 318A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 319A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 320A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 321A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 322A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 323A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 324P; 325P; 326A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; 327P; 328C;
 329A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; and/or 330C.

Claims 3-5 (Canceled).

Claim 6 (Currently Amended). The variant of ~~any one of claims 3-5~~ claim 1, which is a variant of a *Myceliophthora thermophila* galactanase.

Claims 7-9 (Canceled)

Claim 10 (Currently Amended). The variant of ~~any one of claims 7-9~~ claim 1, which is a variant of a *Humicola insolens* galactanase.

Claims 11-13 (Canceled)

Claim 14 (Currently Amended). The variant of ~~any one of claims 11-13~~ claim 1, which is a variant of an *Aspergillus aculeatus* galactanase.

Claims 15-17 (Canceled)

Claim 18 (Currently Amended). The variant of ~~any one of claims 15-17~~ claim 1, which is a variant of a *Bacillus licheniformis* galactanase.

Claim 19 (Currently Amended). The variant of ~~any one of claims 1-18~~ claim 1, wherein the number designating each position is the number of the corresponding amino acid residue in SEQ ID NO: 1, said corresponding amino acid residue being derivable from an alignment according to Fig. 5 or 6, said alignment including the parent galactanase.

Claim 20 (Currently Amended). The variant of ~~any one of claims 1-19~~ claim 1, wherein the parent galactanase has an amino acid sequence which has a degree of identity to the amino acid sequence of SEQ ID NO: 1 of at least 25%.

Claim 21 (Currently Amended). The variant of ~~any one of claims 1-20~~ claim 1, wherein the parent galactanase is obtained from a strain of *Yersinia*, *Aspergillus*, *Humicola*, *Meripilus*, *Myceliophthora*, or *Thermomyces*., or from a strain of *Bacillus*, *Bifidobacterium*, *Cellvibrio*, *Clostridium*, *Pseudomonas*, *Thermotoga*, or *Xanthomonas*.

Claim 22 (Currently Amended). An isolated nucleic acid sequence comprising a nucleic acid sequence which encodes the galactanase variant of ~~any one of claims 1-24~~ claim 1.

Claim 23 (Original). A nucleic acid construct comprising the nucleic acid sequence of claim 22 operably linked to one or more control sequences that direct the production of the galactanase variant in a suitable expression host.

Claim 24 (Original). A recombinant expression vector comprising the nucleic acid construct of claim 23.

Claim 25 (Currently Amended). A recombinant host cell comprising the nucleic acid construct of claim 23 ~~or the vector of claim 24~~.

Claim 26 (Currently Amended). A method for producing a galactanase variant ~~of any one of claims 1-24~~, the method comprising (a) cultivating a recombinant host cell of claim 25; and (b) recovering the polypeptide.

Claims 27 -28 (Canceled).